

Tracing sole juveniles arriving at the Belgian nursery using genomics and otolith shape

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To monitor fish stocks at an ecologically meaningful scale, fisheries management requires to understand population structure. However it is difficult to measure connectivity between populations especially because early-life stages cannot be tagged due to their small size. Success of larval dispersal is the key to connectivity between spawning grounds and nurseries. *Solea solea* is among the most economically valuable fish species in the North Sea, yet little is known about its population dynamics.

In the present study, we investigate the geographical origin of young-of-the-year sole arriving at the Belgian nursery. Previous studies have shown that powerful tools such as genomic markers and otolith shape can reveal fine scale population structure for other fish species. We have sampled monthly in 2013 and 2014 at 13 stations in the southern North Sea. A total of 150 juveniles of sole were genotyped using the double digest Restriction Site-Associated sequencing (ddRADseq) technique.

Three hundred high quality Single Nucleotide Polymorphic sites were retained and used to define population structuring at a fine geographical (<150 km) and temporal scale. Outlier tests were run in order to identify markers that could be used for traceability and might show signatures of local adaptation. In addition to the genetics approach, otolith shape is used in order to reveal small scale population structure. Combining the two different traceability measure increase our assignment power.

We also compared early-life and adult genetic connectivity patterns at the European scale obtained by previous studies. Results show that southern North Sea populations of sole are highly connected, and that those caught off the Belgian coast are closely related to the Eastern English Channel and the Thames estuary populations.

Keywords: connectivity; traceability; early-life stages; flatfish; North Sea; *Solea solea*